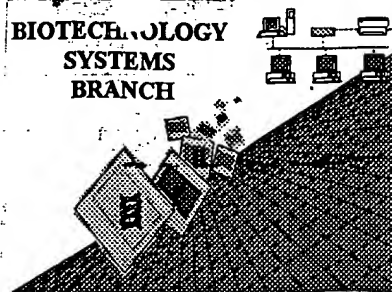# RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/653,755_

Source: _1648_

Date Processed by STIC: _12/4/2000_

RECEIVED
DEC 14 2000
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid-number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

J. PARKIN

1648

RAW SEQUENCE LISTING DATE: 12/04/2000
PATENT APPLICATION: US/09/653,755 TIME: 14:14:25

Input Set : A:\Mab4g10.app
Output Set: N:\CRF3\12042000\I653755.raw

```
       3 <110> APPLICANT: Eisinger, Dominic P.
       4         Stiles, Lynn
       5         LaMarche, Arthur
       6         Jelinek, Thomas
       8 <120> TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for
       9         Phosphotyrosine-Containing Proteins
      11 <130> FILE REFERENCE: 724650-3
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/653,755
C--> 14 <141> CURRENT FILING DATE: 2000-08-10
      16 <160> NUMBER OF SEQ ID NOS: 12
      18 <170> SOFTWARE: PatentIn Ver. 2.1
      20 <210> SEQ ID NO: 1
      21 <211> LENGTH: 1365
      22 <212> TYPE: DNA
      23 <213> ORGANISM: Artificial Sequence
      25 <220> FEATURE:
      26 <223> OTHER INFORMATION: Description of Artificial Sequence:cDNA for heavy
      27         chain of recombinant antibody
      29 <400> SEQUENCE: 1
      30 gaggtccagc tgcarcagtc tggacctgaa ctggtgaagc ctggggcttc agtgatgata 60
      31 tcctgcagga cttctgcata cacattcact gaaaacaccg tgcactgggt gaagcagagc 120
      32 catggagaga gccttgagtg gattggaggt attaatcctt actatggtgg ttctatcttc 180
      33 agcccgaagt tcaaggggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240
      34 atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagaagggct 300
      35 ggggcgtact actttgacta ctggggccaa ggcaccactc tcacagtctc ctcagccaaa 360
      36 acaacacccc catcagtcta tccactggcc cctgggtgtg gagatacaac tggttcctcc 420
      37 gtgactctgg gatgcctggt caagggctac ttccctgagt cagtgactgt gacttggaac 480
      38 tctggatccc tgtccagcag tgtgcacacc ttcccagctc tcctgcagtc tggactctac 540
      39 actatgagca gctcagtgac tgtcccctcc agcacctggc caagtcagac cgtcacctgc 600
      40 agcgttgctc acccagccag cagcaccacg gtggacaaaa aacttgagcc cagcggccc 660
      41 atttcaacaa tcaacccctg tcctccatgc aaggagtgtc acaaatgccc agctcctaac 720
      42 ctcgagggtg gaccatccgt cttcatcttc cctccaaata tcaaggatgt actcatgatc 780
      43 tccctgacac ccaaggtcac gtgtgtggtg gtggatgtga gcgaggatga cccagacgtc 840
      44 cagatcagct ggtttgtgaa caacgtggaa gtacacacag ctcagacaca aacccataga 900
      45 gaggattaca acagtactat ccgggtggtc agcaccctcc ccatccagca ccaggactgg 960
      46 atgagtggca aggagttcaa atgcaaggtc aacaacaaag acctcccatc acccatcgag 1020
      47 agaaccatct caaaaattaa agggctagtc agagctccac aagtatacat cttgcccgcca 1080
      48 ccagcagagc agttgtccag gaaagatgtc agtctcactt gcctggtcgt gggcttcaac 1140
      49 cctggagaca tcagtgtgga gtggaccagc aatgggcata cagaggagaa ctacaaggac 1200
      50 accgcaccag tcctggactc tgacggttct tacttcatat atagcaagct caatatgaaa 1260
      51 acaagcaagt gggagaaaac agattccttc tcatgcaacg tgagacacga gggtctgaaa 1320
      52 aattactacc tgaagaagac catctcccgg tctccgggta aatga       1365
      55 <210> SEQ ID NO: 2
      56 <211> LENGTH: 645
      57 <212> TYPE: DNA
      58 <213> ORGANISM: Artificial Sequence
      60 <220> FEATURE:
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RAW SEQUENCE LISTING                      DATE: 12/04/2000
PATENT APPLICATION:  US/09/653,755        TIME: 14:14:25

Input Set : A:\Mab4g10.app
Output Set: N:\CRF3\12042000\I653755.raw
```

```
 61 <223> OTHER INFORMATION: Description of Artificial Sequence:cDNA for light
 62       chain of recombinant antibody
 64 <400> SEQUENCE: 2
 65 gaaaatgtgc tcacccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 60
 66 atgacctgca ggccagctc aagtgtaagt tccagttact tgcactggta tcggcagaag 120
 67 tcaggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtccct 180
 68 gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagtgtggag 240
 69 gctgaagatg ctgccactta ttactgccag cagtacagtg gttaccggac gttcggtgga 300
 70 ggcaccaagc tggaaatcaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360
 71 tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420
 72 cccagagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggtgtcctg 480
 73 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcaca 540
 74 ttgaccaagg acgagtatga acgacataaa agctatacct gtgaggccac tcacaagaca 600
 75 tcaacttcac ccatcgtcaa gagcttcaac aggaatgagt gttag           645
 78 <210> SEQ ID NO: 3
 79 <211> LENGTH: 1389
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Artificial Sequence
 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: Description of Artificial Sequence:cDNA for heavy
 85       chain of recombinant antibody with 3'-histidine
 86       tag sequence
 88 <400> SEQUENCE: 3
 89 gaggtccagc tgcarcagtc tggacctgaa ctggtgaagc ctggggcttc agtgatgata 60
 90 tcctgcagga cttctgcata cacattcact gaaaacaccg tgcactgggt gaagcagagc 120
 91 catggagaga gccttgagtg gattggaggt attaatcctt actatggtgg ttctatcttc 180
 92 agcccgaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240
 93 atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagaagggct 300
 94 ggggcgtact actttgacta ctggggccaa ggcaccactc tcacagtctc ctcagccaaa 360
 95 acaacacccc catcagtcta tccactggcc cctgggtgtg gagatacaac tggttcctcc 420
 96 gtgactctgg gatgcctggt caagggctac ttccctgagt cagtgactgt gacttggaac 480
 97 tctggatccc tgtccagcag tgtgcacacc ttcccagctc tcctgcagtc tggactctac 540
 98 actatgagca gctcagtgac tgtcccctcc agcacctggc caagtcagac cgtcacctgc 600
 99 agcgttgctc acccagccag cagcaccacg gtggacaaaa aacttgagcc cagcgggccc 660
100 atttcaacaa tcaacccctg tcctccatgc aaggagtgtc acaaatgccc agctcctaac 720
101 ctcgagggtg gaccatccgt cttcatcttc cctccaaata tcaaggatgt actcatgatc 780
102 tcctgacac ccaaggtcac gtgtgtggtg gtggatgtga gcgaggatga cccgacgtc 840
103 cagatcagct ggtttgtgaa caacgtggaa gtacacacag ctcagacaca aacccatiga 900
104 gaggattaca acagtactat ccgggtggtc agcacctcc ccatccagca ccaggactgg 960
105 atgagtggca aggagttcaa atgcaaggtc aacaacaaag acctcccatc acccatcgag 1020
106 agaaccatct caaaaattaa agggctagtc agagctccac aagtatacat cttgccgcca 1080
107 ccagcagagc agttgtccag gaaagatgtc agtctcactt gcctggtcgt gggcttcaac 1140
108 cctggagaca tcagtgtgga gtggaccagc aatgggcata cagaggagaa ctacaaggac 1200
109 accgcaccag tcctggactc tgacggttct tacttcatat atagcaagct caatatgaaa 1260
110 acaagcaagt gggagaaaac agattccttc tcatgcaacg tgagacacga gggtctgaaa 1320
111 aattactacc tgaagaagac catctcccgg tctccgggta aaggtggcca tcaccaccat 1380
112 caccattga                                              1389
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 454
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```
117 <212> TYPE: PRT
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Artificial Sequence:Amino acid
122        sequence for heavy chain of recombinant antibody
124 <400> SEQUENCE: 4
125 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
126   1               5                  10                  15
128 Ser Val Met Ile Ser Cys Arg Thr Ser Ala Tyr Thr Phe Thr Glu Asn
129             20                  25                  30
131 Thr Val His Trp Val Lys Gln Ser His Gly Glu Ser Leu Glu Trp Ile
132         35                  40                  45
134 Gly Gly Ile Asn Pro Tyr Tyr Gly Gly Ser Ile Phe Ser Pro Lys Phe
135       50                  55                  60
137 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
138  65                  70                  75                  80
140 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
141             85                  90                  95
143 Ala Arg Arg Ala Gly Ala Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
144             100                 105                 110
146 Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
147         115                 120                 125
149 Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly
150         130                 135                 140
152 Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp Asn
153 145                 150                 155                 160
155 Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu Gln
156             165                 170                 175
158 Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser Thr
159             180                 185                 190
161 Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala Ser Ser
162         195                 200                 205
164 Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser Thr Ile
165         210                 215                 220
167 Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala Pro Asn
168 225                 230                 235                 240
170 Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile Lys Asp
171             245                 250                 255
173 Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val Asp
174         260                 265                 270
176 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
177         275                 280                 285
179 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
180         290                 295                 300
182 Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Gln His Gln Asp Trp
183 305                 310                 315                 320
185 Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
186             325                 330                 335
188 Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu Val Arg Ala
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RAW SEQUENCE LISTING   DATE: 12/04/2000
PATENT APPLICATION: US/09/653,755   TIME: 14:14:25

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191 Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu Ser Arg Lys
192         355              360              365
194 Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro Gly Asp Ile
195     370              375              380
197 Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn Tyr Lys Asp
198 385              390              395              400
200 Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile Tyr Ser Lys
201             405              410              415
203 Leu Asn Met Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser Phe Ser Cys
204         420              425              430
206 Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys Lys Thr Ile
207     435              440              445
209 Ser Arg Ser Pro Gly Lys
210     450
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 214
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence:Amino acid
220       sequence for light chain of recombinant antibody
222 <400> SEQUENCE: 5
223 Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
224   1              5               10               15
226 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
227         20               25               30
229 Tyr Leu His Trp Tyr Arg Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp
230         35               40               45
232 Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
233     50               55               60
235 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu
236   65              70               75               80
238 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Arg
239             85               90               95
241 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
242         100              105              110
244 Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
245     115              120              125
247 Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Arg Asp Ile
248     130              135              140
250 Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
251 145              150              155              160
253 Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
254         165              170              175
256 Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
257         180              185              190
259 Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
260         195              200              205
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262 Phe Asn Arg Asn Glu Cys
263      210
266 <210> SEQ ID NO: 6
267 <211> LENGTH: 462
268 <212> TYPE: PRT
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence:Amino acid
273       sequence for heavy chain of recombinant antibody
274       with C-terminal histidine tag sequence
276 <400> SEQUENCE: 6
277 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
278  1                   5                  10                  15
280 Ser Val Met Ile Ser Cys Arg Thr Ser Ala Tyr Thr Phe Thr Glu Asn
281              20                  25                  30
283 Thr Val His Trp Val Lys Gln Ser His Gly Glu Ser Leu Glu Trp Ile
284          35                  40                  45
286 Gly Gly Ile Asn Pro Tyr Tyr Gly Gly Ser Ile Phe Ser Pro Lys Phe
287      50                  55                  60
289 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
290  65                  70                  75                  80
292 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
293              85                  90                  95
295 Ala Arg Arg Ala Gly Ala Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
296             100                 105                 110
298 Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
299             115                 120                 125
301 Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly
302             130                 135                 140
304 Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp Asn
305 145                 150                 155                 160
307 Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu Gln
308             165                 170                 175
310 Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser Thr
311             180                 185                 190
313 Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala Ser Ser
314             195                 200                 205
316 Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser Thr Ile
317      210                 215                 220
319 Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala Pro Asn
320 225                 230                 235                 240
322 Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile Lys Asp
323             245                 250                 255
325 Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val Asp
326             260                 265                 270
328 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
329      275                 280                 285
331 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
332      290                 295                 300
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<210> 8
<211> 80
<212> DNA
<213> Artificial Sequence   *see item 12 on Exam Summary Sheet*

<400> 8
gccaccatgg attttctggt gcagattttc agcttcttgc taatcagtgc ctcagttgca 60
atgtccagag gagaaaatgt   80

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Output Set: N:\CRF3\12042000\I653755.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:384 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:384 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: